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Testing phylogenetic algorithms in linguistic databases

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Abstract

© Springer International Publishing Switzerland 2014. Phylogenetic algorithms are a tool that is frequently used in biology and linguistics for reconstruction of the evolution trees for species or languages. However, there is no a definitely superior algorithm: various algorithms have shown the best results in various studies. In this paper we test four most popular algorithms. We make recommendations which algorithm is better to choose in different cases. In particular, the influence of the feasibility of the lexical clock hypothesis is shown. It is shown that the results are also affected by the choice of metric, and that the results can be improved by using the λ-measure instead of the Hamming's measure. The results of the paper are obtained using both the simulation method and real data.

Keywords

Evolution trees, Linguistic databases, Measures, Phylogenetic algorithms